

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

5 (a) a first nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 12, and SEQ ID NO:56;

10 (b) a second nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 8 and SEQ ID NO:28;

15 (c) a third nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide of SEQ ID NO: 16;

(d) a fourth nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to polypeptide of SEQ ID NO: 52;

20 (e) a fifth nucleotide sequence encoding a polypeptide of at least 100 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 14, SEQ ID NO:50, and SEQ ID NO:58;

25 (f) a sixth nucleotide sequence encoding a polypeptide of at least 100 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to SEQ ID NO: 60;

(g) a seventh nucleotide sequence encoding a polypeptide of at least 100 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 4, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, and SEQ ID NO:62;

30 (h) a eighth nucleotide sequence encoding a polypeptide of at least 100 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 18 and SEQ ID NO:20;

35 (i) a ninth nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 26, SEQ ID NO: 34, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:48, and SEQ ID NO:54;

(j) a tenth nucleotide sequence encoding a polypeptide of at least 150 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 32, SEQ ID NO:44, and SEQ ID NO:46;

5 (k) an eleventh nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to SEQ ID NO: 36;

(l) a twelfth nucleotide sequence encoding a polypeptide of at least 200 amino acids that has at least 85% identity based on the Clustal method of alignment when
10 compared to SEQ ID NO: 30; and

(m) a thirteenth nucleotide sequence comprising the complement of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), or (l).

2. The isolated polynucleotide of Claim 1, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID
15 NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, and 61 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, and 62.

3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are
20 DNA.

4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.

5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.

25 6. An isolated host cell comprising the chimeric gene of Claim 5.

7. An isolated host cell comprising an isolated polynucleotide of Claim 1 or Claim 3.

8. The isolated host cell of Claim 7 wherein the isolated host is selected from the group consisting of yeast, bacteria, plant, and virus.

30 9. A virus comprising the isolated polynucleotide of Claim 1.

10. A polypeptide selected from the group consisting of:

(a) a first sequence of at least 50 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 12, and SEQ ID NO:56;

35 (b) a second sequence of at least 50 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 8 and SEQ ID NO:28;

(c) a third sequence of at least 50 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to SEQ ID NO: 16;

(d) a fourth sequence of at least 50 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to SEQ ID NO: 52;

5 (e) a fifth sequence of at least 100 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 14, SEQ ID NO:50, and SEQ ID NO:58;

(f) a sixth sequence of at least 100 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to SEQ ID NO: 60;

10 (g) a seventh sequence of at least 100 amino acids that has at least 90% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 4, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, and SEQ ID NO:62;

15 (h) an eighth sequence of at least 100 amino acids that has at least 95% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 18 and SEQ ID NO:20;

20 (i) a ninth sequence of at least 150 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 26, SEQ ID NO: 34, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:48, and SEQ ID NO:54;

(j) a tenth sequence of at least 150 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NO: 32, SEQ ID NO:44, and SEQ ID NO:46;

25 (k) an eleventh sequence of at least 200 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to SEQ ID NO: 36; and

(l) a twelfth sequence of at least 200 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to SEQ ID NO: 30.

30 11. A method of selecting an isolated polynucleotide that affects the level of expression of a Myb-related transcription factor polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, and 61 and the complement of such
35 nucleotide sequences;

(b) introducing the isolated polynucleotide into a plant cell; and

(c) measuring the level of a polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.

12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, and 61 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, and 62.

13. A method of selecting an isolated polynucleotide that affects the level of expression of a Myb-related transcription factor polypeptide in a plant cell, the method comprising the steps of:

- 10 (a) constructing an isolated polynucleotide of Claim 1;
- (b) introducing the isolated polynucleotide into a plant cell; and
- (c) measuring the level of polypeptide in the plant cell containing the polynucleotide to provide a positive selection means.

14. A method of obtaining a nucleic acid fragment encoding a Myb-related transcription factor polypeptide comprising the steps of:

- 15 (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, and 61 and the complement of such nucleotide sequences; and
- 20 (b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15. A method of obtaining a nucleic acid fragment encoding a Myb-related transcription factor polypeptide comprising the steps of:

- 25 (a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, and 61 and the complement of such nucleotide sequences;
- 30 (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
- (c) isolating the identified DNA clone; and
- (d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

16. An isolated polynucleotide comprising at least one of 30 nucleotides derived from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, and the complement of such sequences.